Instructions to reproduce the workflow of the paper “Modeling Brain Waves as a Mixture of Latent Processes”

**Rcpp main Codes:**

The following cpp codes contains the main functions to generate the MCMC to a periodogram the code also provides detailed description of the parameters used.

* BMARD\_V112020.cpp : main function to fit the BMARD method
* NDPrcpp\_pgramChoudhuri.cpp: Bayesian non-parmetric method of Choudhuri using Bernstein polynomials.

**BMARD fitting to Simulated time series:**

The 3000 (1000X 3 settings described section 3) periodograms fitted can be reproduced with next sentence in a terminal with next shell sentence.

for i in {1..1000}; do Rscript RSCRIPT\_FILE\_NAME $i; done

**Important: Before running, each file indicates how to generate a new simulation or use the simulation data bases in line 46.**

the R file names containing the simulations codes are:

* simulationAR12.R
* simulationmixAR2.R
* simulationMA4.R
* chouduripgramcode.R

**Main Components extraction:**

The BMARD method were run in the simulation using 6 MCMC chains and have to be summarized the following code contains the functions to extract the Maximum A Posteriori estimator of the number of components, the location, scale and weights parameters per chain and globally using all the chains.

* ExtractionBMARDmaincomponentsmodes.R

To accelerate the process the main components extraction was implemented in the HPC cluster with the next job files

In the same way is possible to extract the main components with the ‘for’ shell command for the next files

* extractAR2mixmodes.R
* extractAR22modes.R
* extractMA4modes.R

In the case of the Bernstein polynomials method of Choudhuri (2014) the extraction just computes the pointwise mean, median, and quantile curves using the next R scripts

* ExtractionmeancurvesCHOUDAR2mix.R
* ExtractionmeancurvesCHOUDAR12.R
* ExtractionmeancurvesCHOUDMA4.R

**Figure 2 Reproducibility:**

The following code reproduce Figure 2, Table 1 and Table 2

BMARDcomparison\_Disparity.R

The First section loads the data from the shared matrices

* pgrammatrixAR2.rds
* pgrammatrixAR12.rds
* pgrammatrixMA4.rds

Second section compute the kernel and spline estimator, this should be computed relatively quick.

Third section computes the standardized spectral density function of the three-setting described in section 3.

In section 4 is assumed that all MCMC for BMARD and the Bernstein polynomial method were run and extracted the main components and curves, then load the result data bases corresponding to the extracted main pointwise summary curves (mean, median and quantiles) from the simulations for BMARD and the Bernstein polynomial method of Choudhuri (2014). Then it is necessary locate manually the median of the integrated absolute error (IAE) to finally plot all the curves together using matplot().

**Table 1 and Table 2 reproducibility:**

The last two sections of the code BMARDcomparison\_Disparity.R reproduce Table 1 and Table 2

These tables compute the differences (disparity) of the true values of the parameters specified in the Section 3 for the mixture of AR(2) processes and the location of the peaks of the AR(12) process.

Table 1 then localize the estimation that correctly have at least 3 components and compute the absolute difference between the MAP estimations and the true parameter values, the compute the average and standard deviation for each of the components.

Table 2 only consider the disparity between the true peaks locations and the estimated locations for the 5 peaks of the AR(12) process.